



#6

SEQUENCE LISTING

<110> Schneider, Luke V.
Hall, Michael P.
Petesch, Robert
Target Discovery, Inc.

<120> Mass Defect Labeling for the Determination of Oligomer Sequences

<130> 020444-000710US

<140> US 10/035,349
<141> 2001-10-19

<150> US 60/242,165
<151> 2000-10-19

<150> US 60/242,398
<151> 2000-10-19

<160> 13

<170> PatentIn Ver. 2.1

<210> 1
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:true N-terminal horse apomyoglobin (Myo) sequence

<220>
<221> MOD_RES
<222> (1)
<223> Xaa = Gly labeled with 5-bromo-3-pyridylacetic acid (5-Br-3-PAA)

<400> 1
Xaa Leu Ser Asp Gly Glu
1 5

<210> 2
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:competing 5 residue false sequence, top ranked sequence at five residues

<220>
<221> MOD_RES
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<223> Xaa = Gly labeled with 5-bromo-3-pyridylacetic acid (5-Br-3-PAA)

<400> 2
Xaa Leu Ser Asp Trp
1 5

<210> 3
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:sequence
carrying cloned unknown DNA sequence

<400> 3
tcagtgtctgc tgcaacatgt tacaggaaat 30

<210> 4
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (1)
<223> n = ribosyl adenosine

<220>
<223> Description of Combined DNA/RNA Molecule:M13
origin of replication primer labeled at the 5' end
with ribosyl adenosine

<220>
<223> Description of Artificial Sequence:M13 origin of
replication primer labeled at the 5' end with
ribosyl adenosine

<400> 4
ntgttgcagc agcactga 18

<210> 5
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DNA fragment
from mass ladder produced by chain termination

<400> 5
caatgtcctt ta 12

<210> 6
<211> 11
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA fragment
from mass ladder produced by chain termination

<400> 6

caatgtcctt t

11

<210> 7

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DNA fragment
from mass ladder produced by chain termination

<400> 7

caatgtcctt

10

<210> 8

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:competing 5
residue false sequence, top ranked sequence at
five residues

<400> 8

Gly Leu Ser Asp Trp

1

5

<210> 9

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:true N-terminal
horse apomyoglobin (Myo) sequence

<400> 9

Gly Leu Ser Asp Gly Glu

1

5

<210> 10

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cloned unknown
DNA sequence

<400> 10

gttacaggaa at

12

<210> 11
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:sequence
determined from mass spectral data analysis

<400> 11
atttcctgta ac

12

<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:true ubiquitin
N-terminal sequence

<400> 12
Met Gln Ile Phe Val Lys
1 5

<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:first ranked
competing possibility at fifth residue

<400> 13
Met Gln Ile Phe Arg
1 5